What Can We Learn from Genomically-Driven Trials in Other Tumors?

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Genomically-Driven Oncology Trials

Basket

Test the effect of targeted agents on same genomic alterations across a variety of cancer types



Umbrella

Test the effect of targeted agents on different genomic alterations in a single cancer type







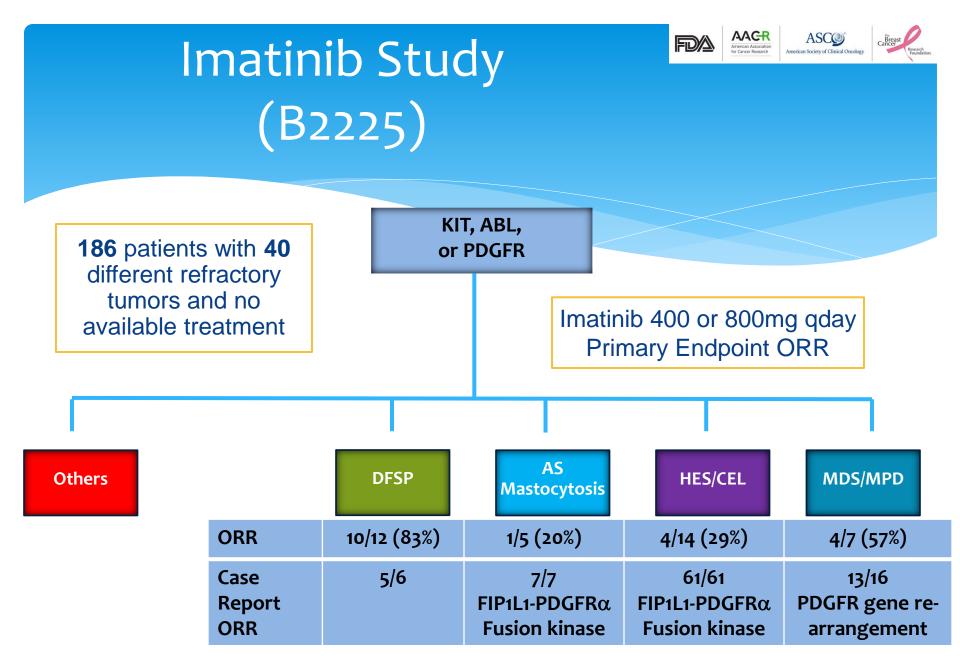




Basket Trials



- ➤ Imatinib (B2225)
- > Pharmaceutical Trials
- > Institution Trials
- > MPACT
- **MATCH**











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Industry Basket Trial Examples









Signature



Refractory metastatic tumor tissue sent for local testing



Result identifies potential target Physician rapidly opens study site



Eligible patient enrolls on targeted clinical trial:

- BKM120 (PanPI3Ki) > Ag
- > TK1258 (FGFRi)
- MEK162 (MEKi)
- **► LGX818 (RAFi)**
- LED225(SMOi)

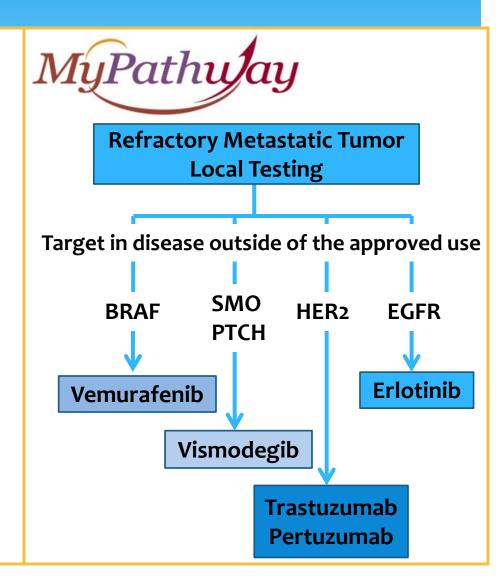
Agents
Planned:

LDK378

LEE011,

BGJ398 and

combinations











Basket Trials



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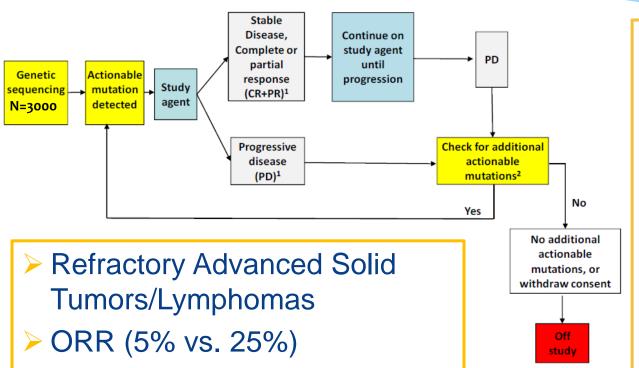






MATCH

(Molecular Analysis for Therapy Choice)



PFS (6 months: 15% vs. 35%)

- Fresh Bx required
- Network CLIA validated labs
- Targeted NGS
- Non-randomized
- Genes/Drugs selected based on levels of evidence
- → 40+ agents pledged with at least RP2D









Umbrella Trials



- ➤ Breast (SAFIR-01)
- Colon (FOCUS-4, ASSIGN)
- Melanoma (GEMM)
- Lung (Lung-MAP, BATTLE, MATRIX, SAFIR-02)
- > Institution Trials











Patient Registration Consent

Tumor Collection

Assign Treatment Arm by Marker

Investigational Targeted Therapy

Genomic Screening

Foundation Medicine NGS Panel

Randomization

Treatment

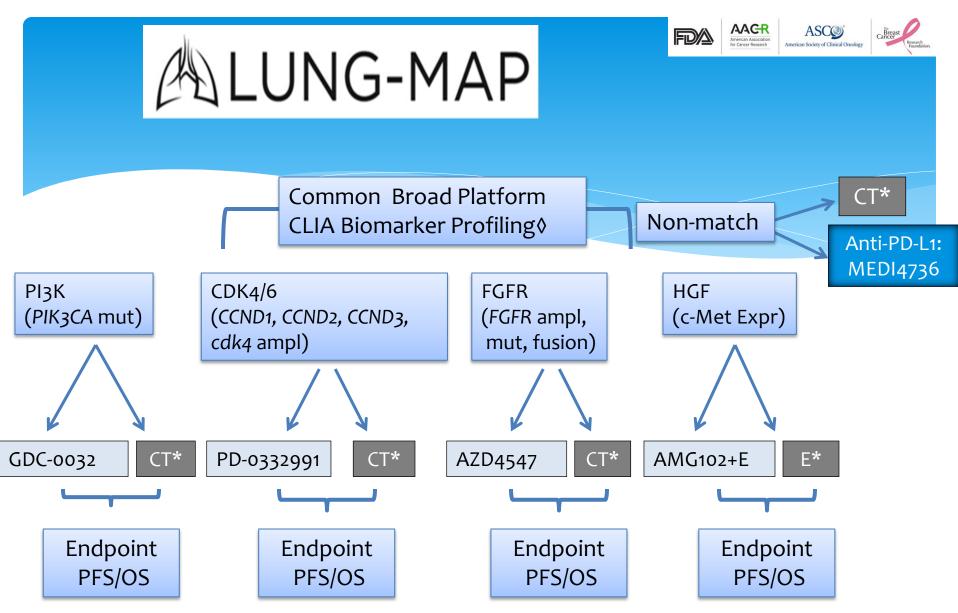
<2weeks

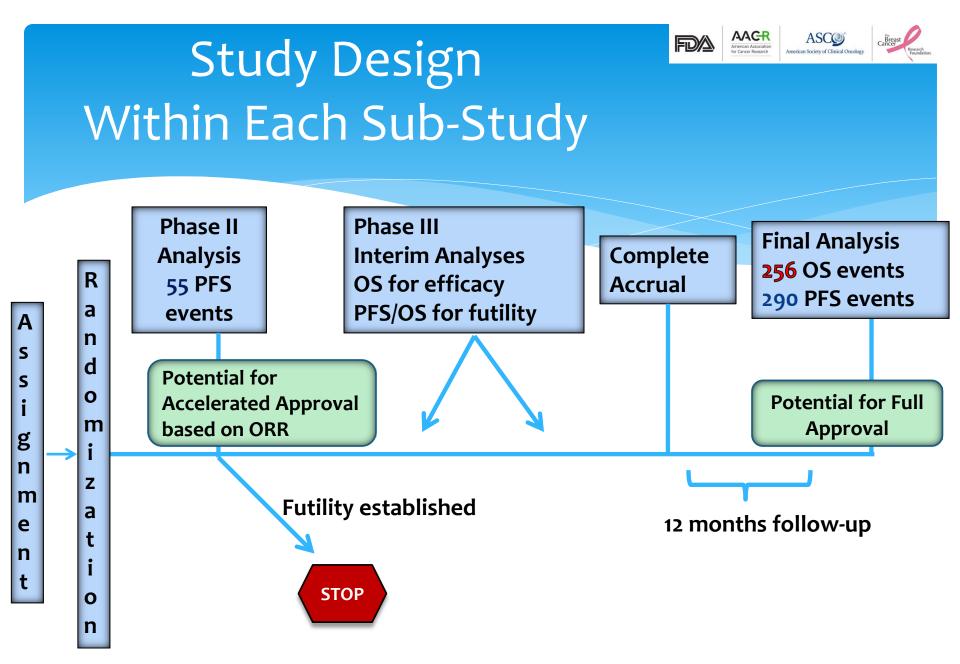
Immunohistochemistry (IHC)

Advanced Squamous Cell Lung Cancer

- Failed platinum regimen
- Measurable disease
- Adequate organ function
- > PS 0-1
- Stable or no brain mets.

Standard of Care Therapy















Sample Size for the Sub-Studies

	Non-match	PI3K	CDK4/6	FGFR	cMET
Prevalence		9%	14%	10%	20%
Assignment Freq.	56%	8%	12%	9%	16%
Phase 2 Size	170	152	124	112	144
Phase 3 Size Analysis	380 21 months	400 72 months	312 45 months	302 53 months	326 37 months
Approx. # needed to screen*	~850	~5,500	~2,700	~3,700	~2,000

^{*}assuming 80% screened will be enrolled











Biomarker-Driven Trial Considerations

Genomics

- * Platform selection
- * Broad vs. targeted screening
- * Central vs. local testing
- * Address heterogeneity
- Assign therapy

Agent Selection

- * Stage of development
 - Investigational (RP2D?)
 - Approved in other malignancy
- * Single agent or combination

Study Design

- * Fresh biopsy vs. prescreen
- * Outcomes/Endpoints
- * Patient population
- * Non-match arm?
- * Data collection
- * Companion Diagnostic
- * Regulatory Goal









Breast Cancer Trial Considerations and Conclusions

- * It is possible to conduct a large genomically-driven trial
- * A registration trial is achievable
- * Many options for genomics/agent selection and design
- * Potential for innovation
- * Cooperation between stakeholders
- * International trial/global collaboration will expedite accrual









Backup Slides

- ☐ Lung-MAP Statistical Design
- ☐ GEMM
- MPACT
- **□** BATTLE
- ☐ SAFIR-01
- ☐ ASSIGN
- □ FOCUS4
- ☐ My Pathway
- ☐ Signature Program
- **□** MATRIX
- ☐ SAFIR-02









Lung-MAP Statistical Design: Phase II Interim Analysis

	Phase II Design		
	Plan A	Plan B	
Primary Outcome	PFS		
Sample Size	55 progression events		
Target HR (% improvement)	HR = 0.5 2-fold increase	HR=0.4 2.5-fold increase	
Power	90%	95%	
Type I error	10%	4%	
Approx. Threshold to conti	nue:		
HR % improvement	HR= 0.71 41% increase	HR = 0.61 63% increase	

Each sub-study can choose between Plan A or Plan B to determine "bar" for continuation past Phase 2 interim analysis









Lung-MAP Statistical Design: Phase III

	PFS and OS Co-primary		
	PFS	OS	
Events	290	256	
Null Hypothesis (HR)	0.75* (33% improvement)	1.0 (equivalence)	
Alternative Hypothesis	0.5 (2-fold increase)	o.67 (50% improvement)	
Type I error (1-sided)	o.014 against HR = 1.33 < o.00001 against HR = 1	0.025	
Power	90%	90%	

^{*} Non HR = 1 null hypothesis encodes clinical significance Sample size based on OS for all studies



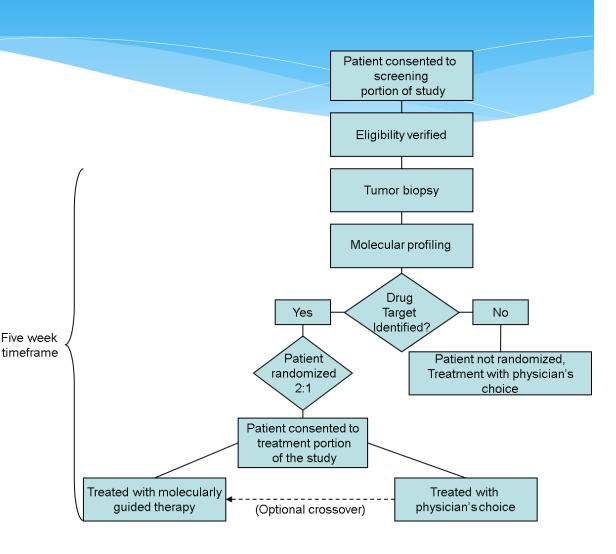






GEMM

- Non-BRAF Mutant Metastatic Melanoma Previously Treated with Immunotherapy
- 136 patients over 18 months for 96 evaluable patients
- Molecular and clinical tumor boards selects therapy



Available Commercial Agents for GEMM:

Drug Name:	Target:	Route
Adriamycin	DNA, TOP2A	IV
Bortezomib-TBD	proteasomes	IV
Carboplatin	DNA	IV
Dacarbazine	POLA2	IV
Dasatinib	C-Src	Oral
Erlotinib	EGFR, NR1I2	Oral
Etoposide	topoisomerase-2	IV
Gemcitabine	RRM1, TYMS, CMPK, DNA	IV
Imatinib	Multikinase (BCR-ABL, c-kit, PDGF-R, RET)	Oral
Interferon, Recomb.	IFNAR2, IFNAR1	Sub-Q
Paclitaxel	TUBB1, BCL2	IV
Pemetrexed	TYMS, ATIC, DHFR, GART	IV
Sorafenib	BRAF, RAF1, VEGFR2, VEGFR3, FLT3, PDGFRB, KIT, FLT4	Oral
Temozolomide	DNA	IV
Vorinostat	pan-histone deacetylase inhibitor	Oral
Inlyta (axitinib)	VEGFR	Oral
Bosulif (bosutinib)	Abl, Src	Oral
Sutent (sunitinib)	PDGFRa, PDGFRb, VEGFR1, VEGFR2, VEGFR3, KIT, FLT3, CSF1R, RET	Oral
Torisel (temsirolimus)	FRAP1	IV
Xalkori (crizotinib)	ALK, ROS1, MET	Oral

Available Investigational Agents for GEMM:

Company Name:	Drug Name:	Target:	Route
Millennium	MLN8237	Aurora A kinase	Oral
	MLN9708	proteasome protease inhibitor	Oral
Pfizer	PF-00299804	pan-erbB	Oral
	PD-0332991	CDK 4/6 inhibitor	Oral
Plexxikon	PLX3397	FMS, Kit and Fit3-ITD	Oral
Exelixis	XL184	Mulit-kinase (VEGFR2, Met, FLT3, Tie2, Kit and Ret)	Oral
Novartis	MEK162	MEK 1/2	Oral
	BGJ398	FGFR 1/2	Oral
GlaxoSmithKline	GSK1120212 (GSK212)	MEK 1/2 (may be used in combination with GSK795)	Oral
	GSK2141795 (GSK795)	AKT (may be used as monotherapy or in combination with GSK212)	Oral



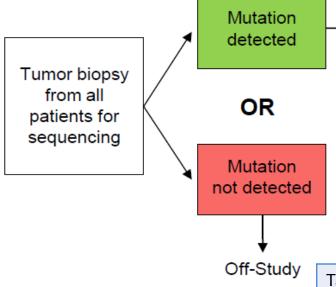




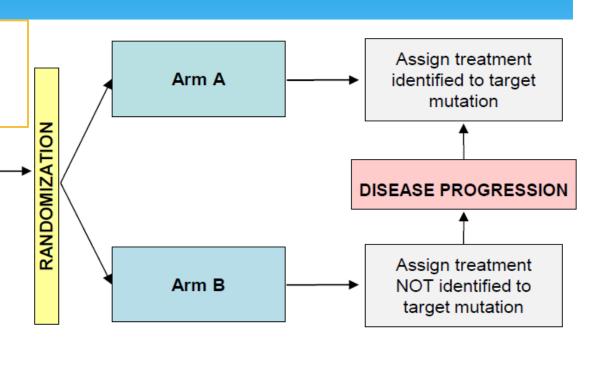


MPACT

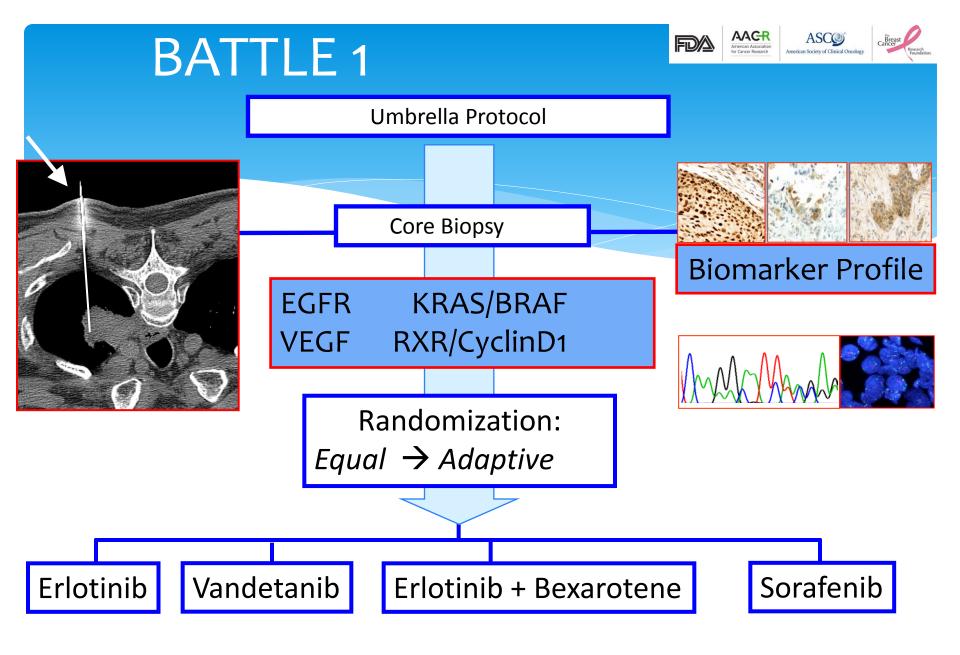
- Refractory solid tumors
- Response rate (CR+ PR) and PFS (4 months)



391 mutations, 20 genes, 3 pathways, 4 treatments



	Target	Therapy
	DNA repair pathway	1. Veliparib (PARPinh) + Temozolomide 2. MK1775 (WEE1inh) + carboplatin
	PI3K pathway, loss of PTEN, Akt Amplification	3. Everolimus
	RAS pathway	4. GSK 1120212 (MEK inhibitor)



Primary end point: 8 week Disease Control (DC)

Courtesy of V. Papadimitrakopoulou Kim E et al AACR 2010

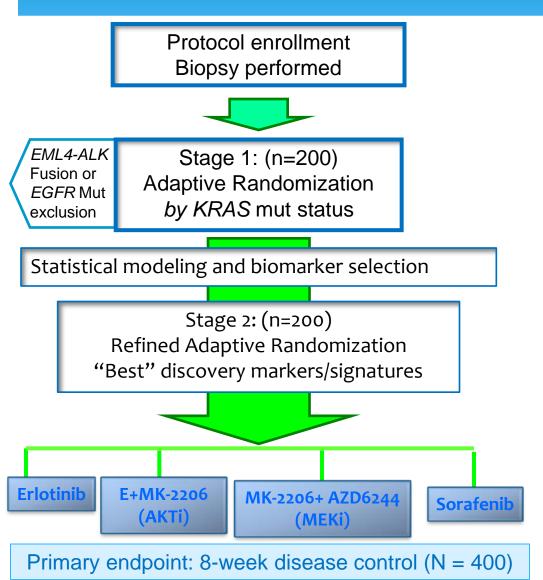








BATTLE-2

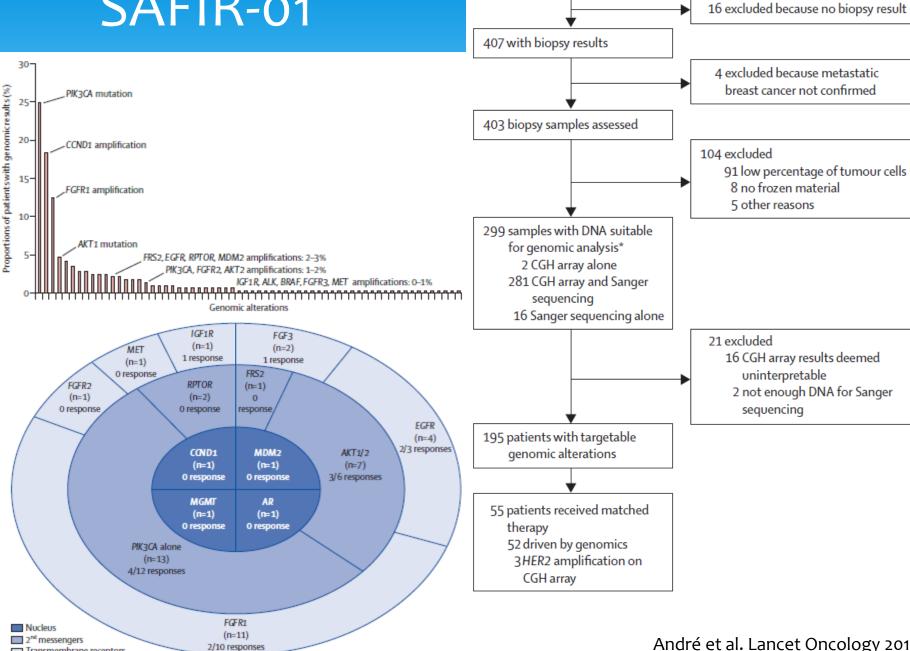


Discovery Markers:

- Protein expression (IHC): ip-AKT (Ser473), PTEN, HIF-1α, LKB1
- Mutation analysis (Sequenom): PI3KCA, BRAF, AKT1, HRAS, NRAS, MAP2K1 (MEK1), MET, CTNNB1, STK11 (LKB1)
- mRNA pathways activation signatures: Affymetrix®
 - BATTLE-1: WT-EGFR-Erlotinib, EMT, and Sorafenib
 - BATTLE-2: new "discovery" signatures
- NGS-Foundation Medicine
- RNA sequencing

SAFIR-01

Transmembrane receptors



423 patients enrolled











Marker Defined
Sub-Groups
(potential options)

CURRENT DESIGN

Consent

Progression on First-line Treatment of Metastatic Colorectal patient to patient to sub-study

Analysis of metastatic tumor specimen

BRAF

RAS

Consent

R)<

Targeted therapy

Targeted therapy

Control arm*

Control arm*

PIK3CA PTEN AKT

R

Targeted therapy
Control arm*

Both RAS and PI3K

R

Targeted therapy
Control arm*

Not RAS Not PI3K

R

Targeted therapy Control arm*

*Standard chemotherapy-containing regimen

Cancer

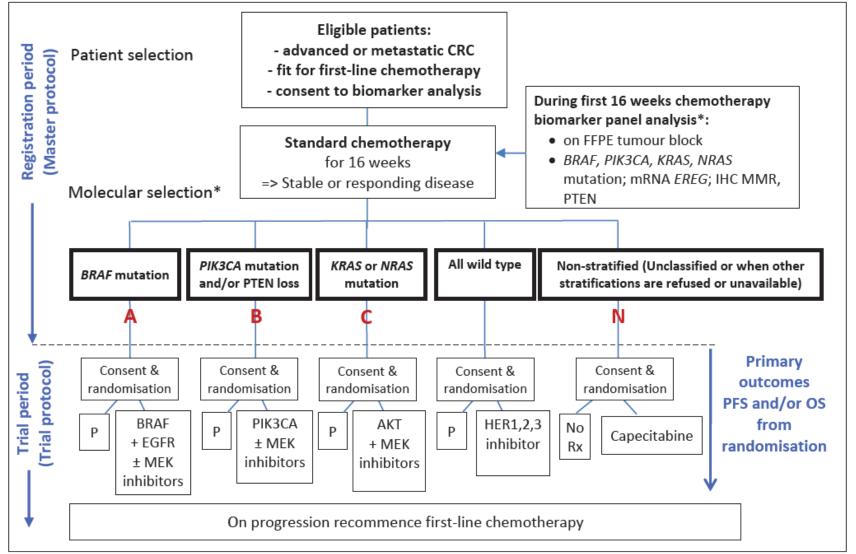








FOCUS4



^{*} The molecular cohorts are arranged in a hierarchy from left to right. For example a patient with both a PIK3CA mutation and a KRAS mutation will be classified into the PIK3CA mutation cohort.

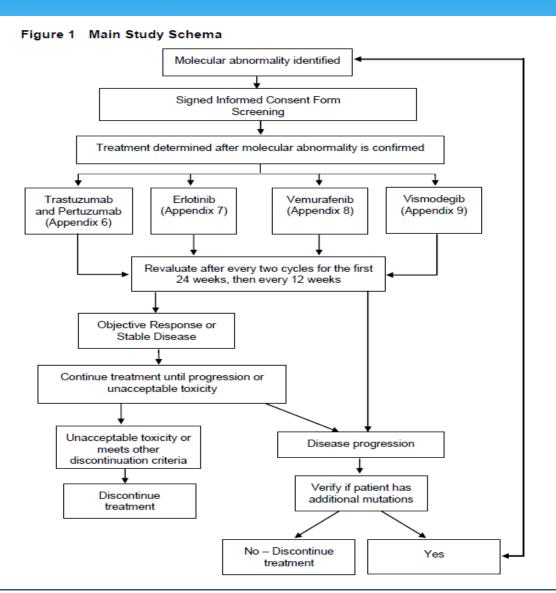








Genentech My Pathway











My Pathway Study Schema

Patients with refractory metastatic cancers with locally determined mutations and/or overexpression that are targets for the drugs in this study outside of the approved use

Standard single agent or combination targeted therapy as follows:

- HER2 amplification, overexpression or mutation: trastuzumab and pertuzumab
- EGFR activating mutation: erlotinib
- BRAF mutation (v6ooe and others): vemurafenib
- Hedgehog pathway activating mutations (Smo/PTCH): vismodegib

Patients with more than one of these abnormalities in their tumor profile will be selected after discussion between the treating physician and the PI based on the mutation considered most critical

Treat until Investigator determined PD or unacceptable toxicity



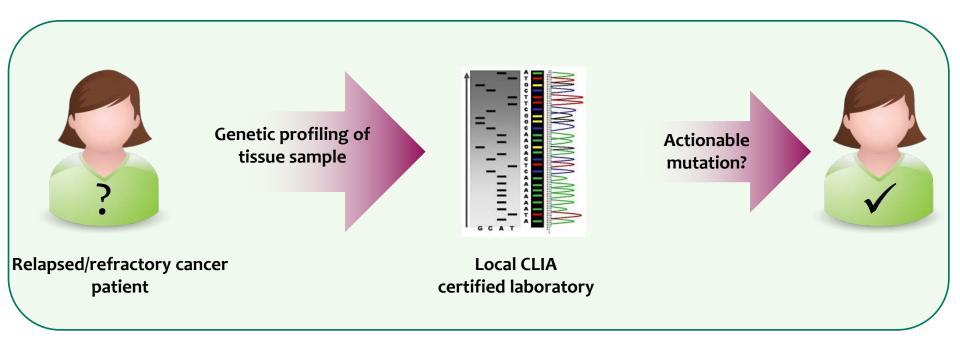






What Is the Signature Program?

- Background
 - The SIGNATURE program rapidly matches patients to treatments that target their tumor's molecular abnormality and brings the trial to the patient rather than the patient traveling to a clinical trial













How Does the Program Work?



Protocol package

- Fixed contract
- Central institutional review board
- Standard budget
- Standard informed consent



When a patient is identified as having an actionable mutation, their oncologist contacts Novartis

Call center prequalifies the patient:

(1) Protocol package sent to site Expedited site visit

(2)

Study open!

■ 5 weeks vs 34-week average



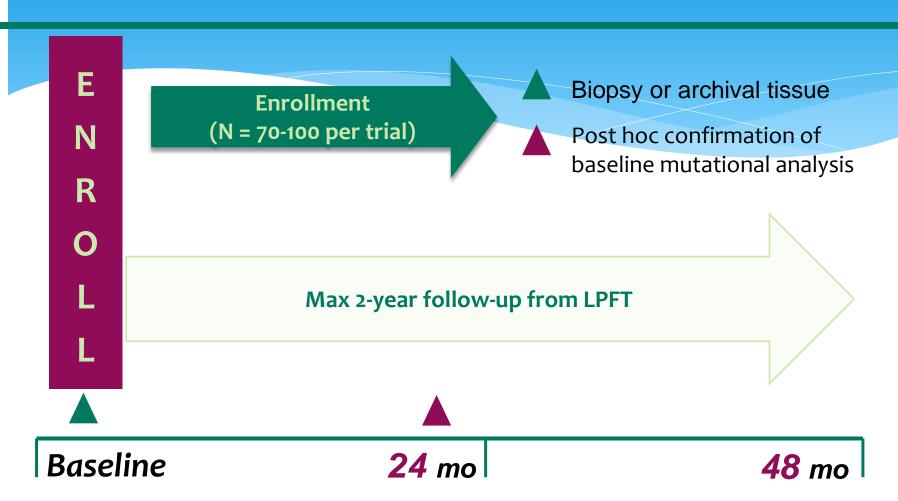








Novartis Signature Study



LPFT, last patient first treatment.



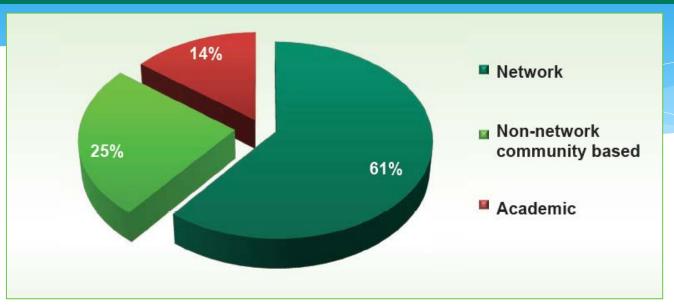








Participating Sites (N = 104)



 Any research-experienced site in the US accepting our study model and with a preidentified patient to participate is eligible

Site Type	Number of Sites (N = 104)	Average Weeks to Trial Start	Patients Dosed (N = 121)
Network	63	3	78
Non-network community based	25	6	16
Academic	16	12	27
Average start-up time across 104 sites = 5.2 weeks			











Signature- Current Compounds Available

- > BKM120 (Pan PI3Ki)
- TK1258 (FGFRi)
- MEK162 (MEKi)
- LGX818 (RAFi)
- > LED225(SMOi)
- Additional Agents Planned (LDK378 LEE011, BGJ398 and combinations)

MATRIX National Lung Trial CRUK

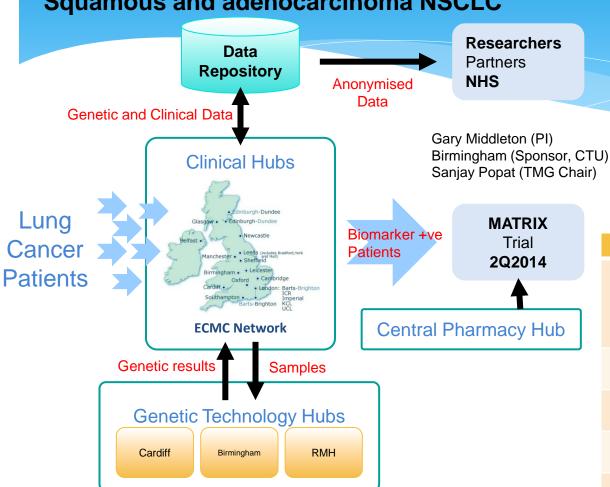








Squamous and adenocarcinoma NSCLC





Compound	Molecular segment	Prevalence
AZD5363	PI3KCA mutation PIK3CA mutation AKT1 mutation PIK3CA amp PTEN null	4.6% 15.2% 0.9% 7.0% 7.9%
AZD4547	FGFR2/3 mutation FGFR2/3 mutation	3.3% 4.4%
AZD2014	LKB1 mutation TSC1/2 mutation	12.2% 8.9%
AZD9291	T790M (Her2 amp)	7.5% (5.0%)
Selumetinib/ docetaxel	KRAS wild type, NF1, NRAS, HRAS mutation	24.9%
MEDI4736	All markers negative (PD-L1 positive)	est. 40%

SAFIR02 Lung Trial – UNICANCER









Squamous and adenocarcinoma NSCLC

